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Deterministic and Stochastic models of SIR Epidemic – A Review

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Abstract

This paper presents a review of mathematical models developed for Epidemics over the past 25 years. The evolution of models of SIR(Susceptible-Infectious-Removed) epidemics which is the classic epidemic model developed for infectious diseases is discussed. Though there are 5000+ articles available in the research arena,it has been taken some of the articles in the past 25 years for the evolution of the refinement of the models over time. Theseselected articles describe the Epidemic models with different situations, problem areas, challenges with different techniques,modellingwith various problem structures and techniques such as discrete time/continuous time state space, transform techniques, Kinetic theory etc. and different distributions of the stochastic variables used. The models have been derived with different techniques,simulation techniques are the common numerical technique in many of the articles for the case studies of interest.

Key words:*SIR Epidemic, Reproduction number, HIV, SARS, Markov chain, Transforms, simulation*

1. Introduction

Worldwide now the situation become panic, the topical discussion everywhere is the effect of spread of Novel Corona virus(COVID-19). Since its nature of creating acute

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respiratory syndrome and the threat accordingly, it is the time to understand thesignificance of disease transmission in structured(compartmental) population. The understanding may be theoretical or practical or mathematical and/or statistical. The researchers are concerned with analysing the qualitative and quantitative way of describing, formulating it as models for epidemics which forecasting the risk of the virus diffusion and for the betterment of the pandemic situation, decision making by the government, human behaviour, the responsibilities to overcome such crisis. Many researchers from 1920, developed mathematical and stochastic models in different aspects. Modelling infectious diseases involve the exaggerated social responses as it exerts with human life. Modelling for epidemics is not as simple as modelling for any other non-infectious diseases as the complexity involved with many parameters in different dimensions

There are two ways of producing models for epidemics, mathematical(deterministic)and stochastic. When the data is so large then deterministic technique which involve differential equations is appropriate whereas stochastic models which engage with Markov chains, branching and diffusion processes are more suitable for low population size. However, if the population parameters exert with many uncertainties, applying stochastic models is more realistic.

The authorsDaley[1], Kolmanovskii[2], Frank BallPeter Neal[3], Krone[4] discussed some models of infectivity, stochastic hereditary systems, great circle and spatial models. Baker[5] discussed the estimation of parameters involved and the appropriate model selection, its properties by Henry[6], Lauren et.al[7] applied network theory in the outbreak of SARS and its optimal control by Xiefei Yan [8], Nirav Dalal[9] modelled for HIV dynamics, Kyriakidis[10] & Daqing Jiang[11] discussed with multidimensional parameters and its long time behaviour respectively.Epidemics with animals [12], Bayesian analysis [13], computer simulation models[14] and determining non trivial solution for rabies epidemic mode[15] are some of the epidemic models discussed in different aspects.

2. Classical SIR Epidemic model

The basic SIR model is that there are $S(i), I(i)\ and\ R(i)$ individuals among the total population considered are in Susceptible, infected and Recovered states respectively. Obviously $S(i) + I(i) + R(i) = N$. There are no births or deaths, but it is termed as

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infection and recovery. The rate of transmission from one state to other states are denoted by $\beta \, and \, \gamma$ respectively from susceptible state to Infectious state and Infectious state to recovered state. The basic differential equations corresponding to these ideas are

$\frac{dS}{dt} = -\beta I \frac{S}{N}$,

$\frac{dI}{dt} = \beta I \frac{S}{N} - \gamma I$ and

$$\frac{dR}{dt} = \gamma I$$

The model is extended with additional phase of infection there by adding additional parameters.

3. Overview of models

There are many stochastic models developed for the HIV epidemic, the homosexual population also considered for many such models. The parameters taken are different in different models as like focusing on the profession, environment, scarcity and starvation. Here one such model analysed by W.-Y. Tan And Z. Xiang[16] by considering the impact of age and race are significant in this HIV epidemic in homosexual population. It has been developed a discrete time stochastic model and extended to continuous time as special case.

The model is explained with stages of spread, the stage 'S' as the suspectable stage, 'L' as the expected stage, 'I' as the infective stage and 'A' as the AIDS stage. Further, the infective stage 'I' split up with many sub stages, say k stages corresponding to the level and duration of infection and therefore there are k+3 stages considered for HIV epidemics.An n dimensional discrete time stochastic process is defined and the model is structured with some assumptions like the mode of spread of the virus (either by sexual contact or by blood transfusion), due to the awareness of HIV virus, the rate of affected people having sex partners with other non-affected people would be low & their change of behaviour of sexual activities may lessen the sexual activity level, the symptoms occurred for those who are affected with other diseases like ELISA, Western blot, bacterium tuberculosis, cervic cancer(for women) etc. may affect the rate of transmission for i^{th} stage of I to stage S, the transition rate at any time t would be considering all these assumptions.To find the probability distribution of the number of sexual partners, it is appropriate to use the negative binomial distribution and the normalising conditions to the model have been defined and tested. Further the

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chain multinomial model which is the extension of chain binomial has been applied with the two steps, first by deriving the probability that the virus affecting the people, second to move from the states of the stochastic model and the chain multinomial distribution has been derived.Further, the discrete time stochastic model is extended to continuous time model by partitioning the time interval into some non-overlapping subintervals. To illustrate the results numerically and visually, computer simulation studies have been made.

Sleeman[17] discussed a non-linear stochastic model for AIDS Epidemic for both homosexuals and bisexuals admit heterogeneous risk behaviour when the delayed report occurs in philadelphia's public health data. Since such Epidemic involves many parameters with different risk categories and transitions within the categories lead to multi dimension parameter areas. The evolution of the embedded non-linear stochastic models is suitable for such areas, which was in turn automated with software development. In the stochastic model process, a set of non-linear differential equations corresponding to different risk behaviour among the population have been formulated, applying Monte-carlo methods experiments through simulation and the results of the experiments are assessed with the corresponding parameter estimates found by deterministic models.

Robert and Saha [18] produced a simple model for the epidemic with stochastic parameters. They considered the disease transmission rate and the proportion in which the people(animals) infected with the population as a stochastic random variable, defining the population density and its birth and death rates.to frame the differential equations corresponding to these parameters, a one dimensional stochastic model is taken into account with the parameters increase in mortality rate, the probability of vertical transmission, the disease transmission rate, contact rate between individuals and so on. They produced a logistic differential equation and solve its probability density function. The first and second moment of the distribution have been found directly from the differential equations and thereby found the stochastic measures mean and variance. The analysis concluded that the variance is below the critical value which have been derived in this model in which the disease may be prevented whereas if the variance is above the critical value the disease would be eradicated.

Blount and Yakowitz[19] described an intractable stochastic model for epidemic. The various stages of the infectious disease (HIV) were described as compartmental Markov model. As the transition from one stage to another stage lead to nonlinear

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functions, the numerical solution of Chapman-Kolmogorov equations is found rather the expected parameters of the transition. For the computation of the model, the probability vector matrix (PVM) has been defined which is appropriate for the epidemic models with large in population. This PVMs are then correlated to SI (susceptible and infected) epidemics and its corresponding probabilities have been computed. An illustrative example is discussed with HIV/AIDS model.

In the computation of Epidemic measures, an important approach made by USA in AIDS projection through the centre for disease control prevention is the back calculation otherwise called back projection which has a drawback of non-focusing of the virus's dynamic nature. To incorporate such dynamic aspects, Hulim[20] considered the state space which are used to find the past and future states of HIV epidemics include both infectious and suspicious people. The SIA (susceptible-infected-AIDS) descriptions with different infected levels have been considered, with the results obtained, further extended to a state space multinomial model and the method has been illustrated with the Sanfrancisco homosexual population.

In the earlier models, most of the articles deal with single group/ multi group and epidemiologic and or demographic models, the classification about the infectious stages of the epidemic with incubation period, age, heterogeneity, models with identification of factors which affect the spread of HIV virus through sexual contact or blood related transmission and sharing of drugs. Here Feng et.al[21] considered the virus which is not a single type virus with different sequential stages of infection classified the virus into parental and recombinant or mosaic virus. It is from the fact that a virus can be infected with two or more proviruses, encapsidation of one RNA from each provirus to create a new recombinant virus. Between the two recombinant RNA, a newly fused DNA sequence which is recombinant, is moved back and forth between the source genomes. A model is framed with the discrete breakpoints between genomic spaces with various phylogenetic relations. This is from the fact and statistics that in south Africa, it has been identified A clade and D clade viruses which are commonly spread over the population, later there are A/D combinant viruses identified in the same region. The recombinant viruses combine again with its parental virus type or a different subtype. To classify and evolute the recombinating effects of the viruses, the model has been derived for two kinds, one is for parental viruses and other for recombinantal or mosaic viruses.In this article, there are exactly two kinds of parental viruses considered, The infectious population corresponding to

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parental viruses and the mosaic virus are taken as $V_1, V_2 \, and \, V_3$ respectively, considering the stochastic parameters corresponding to the interaction(co efficient) between the parental viruses, between the parental and recombinant, the parameter to the probability of recombination, growth rate in each subtype, the differential equations of transmission have been derived. The stability of equilibria, global structure and the main results of the model have been analysed.

To describe the evolution of epidemic, Delitala [22] applied the kinetic theory approach to model epidemic. Kinetic theory is the one which includes mixture of states in various underlying parameters involved in the evolution of epidemic. Here the epidemic mathematical model is designed kinetic theory considering the very big system of many ways of interactions among the population which involve not only the geometric variables and mechanical variables but also involve the sociobiological state variable.The work is divided into four parts,introducing the model with the kinetic theory approach, describing the model with the state space (the stochastic model is a phenomenological model in which the evolution equations which are usually framed with microscopic observation based on individual's interaction have been considered for phenomenological terms based on macroscopic observations), derived the equations for the spatially homogenous case, simplify it and generalise for more extended models which can further be used for any epidemic and finally the microscopic interactions have been analysed to find the transition function and epidemiological model and its perspectives have been discussed.

The virus SARS (Severe Acute Respiratory Syndrome) which is transmitted from single individual to many which is termed as SSE(Super Spread Event) influenced and encouraged many epidemiological studies. Michael[23] produced a mathematical model for the transmission of SARS considering in two ways, the transmission occurs to the immediate neighbours and the random spread of its geographically located region. He classified the infectious people into four categories SPIR(susceptible Prone Infected Removed) with its conventional definitions with the state transition graph is

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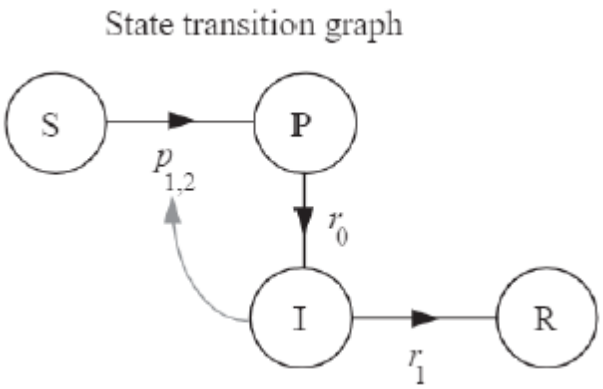

where p_1, p_2, r_0 and r_1 are the transition probabilities from one stage to another stage. A numerical analysis is carrid out with a case studies and found an analytic result for the expected number of new infections and the expected number that an infected person will spread to new cases everyday.

John[24] considered the network of population over disease transmission as the scale free network in which its number related with the number of connections it has to other nodes in a network and its probability distribution follows power law which is the change in one quantity of population results in a proportional change in other quantities irrespective of the size of the population. Such networks allow the structured population, while modelling epidemic it reduces the complexity of transmission. He analysed an empirical and deterministic model to find the rate of time dependent epidemic for structured and unstructured population and find the stochastic measures that employ the controlling of disease transmission and the outbreaks.

Sen-Zhong[25] produced a new SEIR model which is the refined model of classical SEIR which includes the vaccination process which eradicates the disease and the possibility of emerging new infections can be controlled by quarantining the suspected cases, introducing the measure R_0 which is the basic reproductive number for the contagious diseases which is the key parameter which controls the entire epidemic.

The parameters involved in this model are very wide, some of them are vaccine efficacy against susceptibility/infectious, the immunisation threshold. The disease transmission pattern has been divided into four categories, light, moderate, severe and extremely severe which are denoted as type I, II, III and IV respectively. With the usual notation that the mean infectious period and the mean infection rate , the reproductive numbers associated with the four types of transmission have been

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derived and the impact on the vaccination controls the epidemic analysed. There are four methods discussed to calculate R_0 , the estimation of parameters are encountered and the results have been compared for several diseases such as chicken pox, Diphtheria, Fifth disease, Hepatitis B, HFMD, Influenza, measles, mums, pertusia, polio, Rubella, scarlet fever, small pox, HIV, SARS, Ebola, AHC, FMD, Avian influenza, HIV and SIV. The model has been elaborately explained for different cases, the range of R_0 for all the familiar infectious diseases calculated using this model agree with the corresponding values calculated by the usual methods for the specific observed data.

Guinness[26] developed a mathematical model framing deterministic ordinary differential equations(ODE) which include the additional biological parameters. To destroy an infected cells the CD4+T cells which are the essential blood white cells of immune system send signals to other cells who kill the infected cells have the possibility of being infected, but during vaccination or drug treatment, it would target the HIV infection and viral load may fail to taking care of such killer cells like CD4+T, macrophage, Dentritic etc.and they proceed producing virus. The conventional methods do not include such parameters into account as the more the parameters the more the dimension which increase the complexity of the models and only few key roles are considered. This model focusing on such parameters, using dimensional analysis addition additional biological features into the differential equations, and thus a two type of ODE analysis correspond to single cell and multi cell versions are analysed. Single cell models derive the differential equations of the linear model for the overall nonlinear biological system, modelled the transmission of the CD4+T cells and the HIV infected cells and thereby constructing the delay differential equations correspond to the infection delay(the infected cell takes more than 10 hours to produce HIV virus) and extended to multi cell analysis. Applying dimensional analysis will reduce the number of parameters considerably with the accuracy preserved. Without loss of the biological realism and the related key factors, this model has been incorporated and access the impacts occurred in the progression of diseases.

Jan[27] applied the concept of assimilation of data techniques for SIR epidemic model. Data assimilation is the technique of producing data by the sequential statistical estimations. One classic data assimilation is the Ensemble Kalman Filter(EnKF), but this method is appropriate in large range data process thereby

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increasing the amount of computations, an additional local process is needed to reduce the complexity of manipulating with the co variance matrix. For this purpose, the author has proposed Fast Fourier Transform (FFT) invoked KnKF. The idea behind this FFT KnKF is it considers distance vector and its function corresponds to the co variance between two nodes and the product of the covariance matrix and the vector becomes the convolution function.FFT KnKF uses very small ensemble but greater than one, however it is same for one dimensional or any n dimensional case. There is a morphing transformation of KnKF transforms the ensemble member to the state vector and the inverse morphing transforms obtain the ensemble members. It has been concluded that the conventional KnKF or morphing KnKF have some lacking in moving the state towards the data but the morphing FFT KnKF would do it better.

Fabio et.al[28] discussed the classical SIR and SIRS models with Partial Differential Equations approach. He applied hyperbolic Kolmogorov equations which consists of SIR and ordinary differential equations as its characteristics. The model is analysed with structured population which is the well-known compartmental model, with the conventional notations of the epidemic model. This model used very fundamental concepts and results of PDE, but unlike ODE, this PDE approach may lead to the analysis in continuous dynamics which includes many parameters of interest which are in need over time.

Alison[29] et.al produced the SIS epidemic model with two state Markovian chain model and applied computer simulations to find the explicit solution. For this he started with Predator-Prey Lotka Volterra model correspond to the environmental noise which influence the population system. A finite state Markov chain is defined with the characteristics of this equation and a stochastic Markov model has been classified for SIS epidemics. He started with basic stochastic differential equation for the deterministic epidemic model with the usual parameters defined in all the other models of this article. The environmental noises are then compared with effect of changes made by the parameters $\alpha, \beta \; and \; \gamma$ in SIS model, then this will be converted as stochastic epidemic model with Markovian switching will replace all parameters as the finite state space Markov chain. The reproduction number R_0, the extinction and/or persistence probabilities are carried out the simulation technique applied for case studies.

Maoxing [30] discussed the SIS epidemic model for delayed spreading of disease is considered. Due to awareness created, people may follow to distancing which may

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deplete the risk of the spread of infection. The time delay is with some threshold and the delay differential equations are derived. If the reproduction number $R_0$is less than 1 then there is a possibility to eradicate the disease completely but stays when it is greater than 1. With this the model estimated the slowly oscillatory periodic solutions in which the oscillatory measures are found by the time delay. with its fundamental equations the results of equilibria and oscillation have been derived.

Artalejo[31] discussed elaborately the SIR epidemic model with a classical stochastic birth death process. With the standard SIR model definition, he refers the birth rate (λ) as the infective rate, the death rate (μ) as the recovery rate, the continuous time Markov chain to describe the dynamic and epidemic of the process and derived the epidemic descriptors and its probability distributions. The model described for unidimensional birth death process and left the remarks for bidimensional SIR with simple algebraic easier for computations. The Laplace and its inverse are applied for finding the time distribution to reach the individual run of infections. He finds the final size which is the number of affected populations who were infected on at least one occasion in the epidemic with the bidimensional continuous time Markov chain. DefiningMarkov generator matrix, the number of subsequent infections for a particular individual taken into consideration is derived with the finite state space, single absorption state and the transition matrix for states of different individuals. The time distribution to reach the specific state, to reach a critical number of infections are also derived. Numerical results are provided and discussed for the behavioural analysis of the model.

Chen et.al[32] discussed a simple mathematical model for any infectious disease. He considers some parameters like logistics, vaccination, states of transmission, disease progression, recovery rate etc. The number of individuals affected with the disease over the period of time and the drug treatment needs for recovering them are computed numerically with case studies. The model is described as SLAIRD(Susceptible-Latent-Infecious-Isolated-Immune/Recover-Dead), the states, transmissions and the status of the diseases and the infected individuals are shown in flow diagram.A discrete time mathematical formulation for the logistic responses engage the disease progression, vaccination through which impact with the logistic deployment, the amount infected people in different stages and the medical needs in each period is done. This model is concerned with the logistic related questions to make the better decision making, about the way in which the antibiotics and antiviral

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drugs prescribed, whether the drugs prescribed are throughout the infection period or varies with infection stages, the inventory of the vaccines and the resources(hospitals) and many more.

Mattia[33] considers the discrete time SIR, derived a set of discrete time moment equations at the individual and pairs of nodes for the probability of the system states. First he introduced the network as a graph in which its vertex set is the set of individuals and the edges are the connection between them. The model assumes discrete time moments all the parameters corresponding to the conventional SIR models are represented with time parameters, the probabilities of transmission of susceptible to infectious state and infectious to recovered state respectively and the analytical solution for these probabilities have been derived appropriately.

Linda[34] has given a classical representation of epidemic model for the beginners, the descriptions, formulation, derivation and the numerical analysis. He started with three fundamental deterministic differential equation governing with the states of SIR model with the equilibrium condition. And he extended the same equations for the continuous time Markov chain, explaining the well-known forward backward Kolmogorov equations corresponding to the differential equation of probabilities. He then referred the branching process approximation which is a birth death process applies to CTMC models for the disease-free equilibrium in which for some cases this branching approximation lead to exponential growth or tend to zero and a brief concepts and formulation of few more characteristics like extinction and the parameter R_0 – the reproduction number and the threshold parameter. Numerical simulation is made and a case study for Malaria is discussed.

Muhammad et.al[35] discussed the SIR model with fractional differential equations. He has considered the standard compartmental model along with the differential equations which were discussed in the previous models and he used the two existing definitions for Riemann Lioville fractional integration of a function f to find the results for fractional differential equations. An approximate solution of thisnonlinear FD equations by using Laplace Adomian decomposition method has been determined. The stability condition and equilibrium has been analysed by means of disease-free equilibrium, threshold number and the reproduction number R_0. Differential transform method is presented for comparative study with the existing non-linear equation method and the classic methods.

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Getachew[36] discussed a stochastic model for giving stochastic optimal control measures for the re-habitalising and recovering of obioid addicts with some intervention policies. He has formulated an asymptotic exit control problem, mathematical descriptions and assumptions made to find the solutions of optimizing the problem and a constructive example as case studies is taken for analysing the results. With the usual notation of Susceptible Infectious and Recovered model parameters, he has included the one-dimensional Brownian motion, formulated as controlled eigen value problem, characterised for the optimum exit control problem and concluded that while applying random processes as perturbation, it can be extended to fixed characteristics of perturbations, more stochastic information can be added for the better interpretation of the outcome of the model.

A stochastic model Approximate Bayesian Computation (ABC) is used by Amanda[37] to fit for the infectious disease model which require the accuracy and time efficient. Since this method involved with random variables, the results obtained for the probability distributions and the Sequential Monte Carlo(SMC) techniques applied in this model to estimate the parameter values with more accuracy. It has been discussed the basic ABC algorithm and ABC rejection algorithm, the acceptance and rejection are subject to some threshold c and a case study is made with the ABC rejection algorithm implemented in R.

Sarbiit et.al[38] developed an epidemic model for the outbreak of COVID-19 to analyse and predict the death count with the information about the dynamic nature of the virus. So many such analysis have been made by various authors using mathematical or stochastic models which are dealt with the linear equations with simple dimension. For making a time series analysis in nonlinear models with multi scale including more parameters of interest, it is appropriate to choose wavelet transforms. The wavelet function analyses a non-periodic and transient signal. It is noted that the Autoregressive Integrated Moving Average (ARIMA) model is the best to use the past values to predict the future values. ARIMA model along with wavelet transform technique applied in linear and nonlinear data which can be the best to forecast the performance measures.

Kuangang Fan[39] proposed the nonlinear model for stochastic epidemic. Considering the differential equations to the SIR model along with other parameters such as infectious rate, recovering rate and all, here is taken the effects medication and Levy jumps for consideration. The characteristics such as noise intensity is

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considered and with this it has been concluded that the recovering rate after proper vaccination process influence the measures of extinction and persistence.

Conclusion

Review articles are elaborating the overall structure of the research on the area of interest. Epidemic situation analysis with its theoretical back round, decision making, treatment strategies and many other related things can never be complete without the influence of the analysis made with numerical data and probabilistic values of the parameters involved. The models may be designed with the accurate statistics or random data, the associated models determine the measures with analytical and/or numerical results. The unique situation deals with a unique model either deterministic or stochastic with an appropriate method to derive and solve the mathematical formulation of the problem. In this article, it has been discussed with different models with different infectious situations such as SIR, SIER etc. and infectious virus such as SARS, HIV etc. The study and analysis of appropriate model for a suitable situation will enhance the researchers to select the best fit in modelling for epidemics.

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